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                                                                                                                                           Submitted (08 MAR-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest&sanger.ac.uk
On Sep 12, 1999 this sequence version replaced gi:5734384.
IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments snot known; 800 n's separate segments. Contig_ID: 00741 Length: 112424bp.
* MOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 112424)
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Submitted (27-NOV-1996) Biochemistry, University of Missouri, 117
Schweitzer Hall, Columbia, MO 65211, USA
Location/Qualifiers
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KVMNAQKAGASAVLVADDIEEPLITMOTPEEDVGSAKYIBATI ISALIGKSFGEKLK
DAIGGGDWYNVHLDWERAVHPBODREYELWINSNDEGGVKODLIEFLJEKSFGEKLK
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CFKGDGYTTCEYGGHGRCKINNGGCWDCKTANIAACKDTFEGRVECCPLVGGV
QFKGDGYTTCEYGGHGRCKINNGGCWHDARNGHAFSACLDDGYKCQCPAGFKGDGVK
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55 a 306 c 518 g 552 t
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Search completed: September 20, 2000, 08:24:58 Job time: 21038 sec

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CDS	/gene="hADV38S2" join(3400034048,34298>34597) /gene="hADV38S2"
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repeat_	_region
Query Match Best Local Matches 1	Match 78.3%; Score 18; DB 11; Length 247877; Local Similarity 100.0%; Pred. No. 98; es 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 to Db 16981 TO	tcaggtatgtgatttcaa 19
PESULT 14 PSU79958 LOCUS DEFINITION ACCESSION VERSION	PSU79958 1931 bp mRNA PLN 06-OCT-1997 Pisum sativum BP-80 vacuolar sorting receptor mRNA, complete cds. U79958 1 GI:1737221
SOURCE ORGANISM	pea. pea. pea. Pisum sativum pis
REFERENCE	Plsum. 1 (bases 1 to 1931) Kirsch,T., Paris,N., Butler,J.M., Beevers,L. and Rogers,J.C.

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Refrich, T., Paris, N., Butler, J.M., Beevers, L. and Royers, J. C.

Purification and initial characterization of a potential plant
vacuolar targeting receptor

Proc. Natl. Acad. Sci. U.S.A. 91 (8), 3403-3407 (1994)

Py4211872

E (bases 1 to 1931)

E 2 (bases 1 to 1931)

Paris, N., Rogers, S.W., Jiang, L., Kirsch, T., Beevers, L.,

Phillips, T.E. and Rogers, J.C.

Molecular cloning and further characterization of a probable plant
vacuolar sorting receptor

Vacuolar Sorting Rogers, S.W. and Rogers, J.C.

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Paris, N., Rogers, S.W. and Rogers, J.C.
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intron

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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rockville, MD, USA
This sequence was identified as CDM:10211864 by
                                                                                                                                                                                                                                                                                                                                                                                        For further information on this sequence e-mail to flyecelera.com.

* NOTE: This is a 'working draft' sequence.

* This sequence as this sequence and thished sequence as soon as it is available and by the fillished sequence as soon as it is available and the accession number will be preserved.
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HMRVHGNNNSSNGSNGATGVGGESSTGSGVGGGNSLLT."
5194. _5481
Score 16.8; DB 42; Length 81901; pred. No. 41;
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Muscomorpha; Ephydroidea; Drosophilade; Drosophila.

Editor (Champe M. Chawze, C., Chew, M., Ciesiolka, L., Rotenhoff, C., Champe M., Chawze, C., Chew, M., Ciesiolka, L., Butenhoff, C., Champe M., Chawze, C., Chew, M., Karra, K., Kearney, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Doyle, C.M., Farfan, N.A., Hummasti, S.R., Karra, K., Kearney, L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Moshrefi, B., Poon, L., Sequelara, A., Sethi, H., Snir, E., Moshrefi, B., Poon, L., Sequelara, A., Sethi, H., Snir, E., Spirks, S.R.R., Man, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and Ponda, R., Man, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and Ponda, R., Man, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and Ponda, R., Man, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and Ponda, R., Man, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and Ponda, R., Man, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and Ponda, R., Man, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and Ponda, R., Man, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and Ponda, R., Man, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and Ponda, R., Man, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and Ponda, R., Man, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and Ponda, R., Man, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and Ponda, R., Man, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and Ponda, R., Man, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and Ponda, R., Man, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and Ponda, R., Man, K.H., Weinburg, T., Zhang, R., Zie
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Direct Submission

Direct Submission

Submitted (22-JUN-1999) Drosophila Genome Center, Lawrence Berkeley

Experimental (22-JUN-1999) Drosophila Genome Center, Lawrence Berkeley

Laboratory; MS 64-121, Berkeley, CA 94700, USA

For further information about this sequence, Including its location

on Sep 3, 1999 this sequence version replaced email

and relationship to other sequences, Please visit our sequence

archive Web site (http://www.fruitfly.org/sequence/) or send email

archive Web site (http://www.fruitfly.org/
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LULU/890 LZ1256 bp DNA

HTG BACR02G21 (D722) RPCI-98

Drosophila melanogaster chromosome 3 clone BACR02G21 (D722) RPCI-98

A** R0 Importance nicon
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1059: gap of unknown length
1580: contig of 521 bp in length
1660: gap of unknown length
2367: contig of 707 bp in length
2347: gap of unknown length
3319: contig of 872 bp in length
3399: gap of unknown length
4062: contig of 663 bp in length
4142: gap of unknown length
4142: gap of unknown length
5113: contig of 6791 bp in length
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ORIGIN BASE COUNT

2857

2226 c

2220 g

2651 t

exon

/gene="gl"

/db_xref="FlyBase:FBgn0004618"

number-

/db_xref="FlyBase:FBgn0004618"

'gene="gl" 'number= 'gene≖"g]

intron

Query Match Best Local Similarity

Matches

18;

Conservative

90.0%;

Score 16.8; 1 Pred. No. 42;

DB 33; 2;

Mismatches

밁

7129 CCTGGGCTTAAGTCTATCCG 7148

1 cttgggcttacgtctatccg 20

RESULT

AC014473/c

REFERENCE AUTHORS TITLE JOURNAL

Adams, M. and Venter, J.C. pirect submission

COMMENT

BASE COUNT ORIGIN

22813 a

).organism="Drosophila melanogaster" /db_xref="taxon:7227" /db_xref="taxon 7227" / 17895 c 18046 g 23147 t

were Match

30.08;

FEATURES

source

SOURCE ORGANISM

KEYWORDS

ZERSION

HTG; HTGS_PHASE2

AC014473.1 GI:6436862

SSION

MOLLI

Drosophila melanogaster,

81901 bp

AC014473

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DEFINITION
ACCESSION
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KEYWORDS

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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea;
                                       glass gene, transcription factor; zinc finger protein. fruit fly.
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                                                                   Drosophila glass gene encoding a zinc finger protein.
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                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (14-JAN-1999) HHMI, Stanford, Beckman Center B271, Stanford, CA 94305-5323, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryot; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 9085)
Gunn,T.M., Miller,K.A., He,L., Hyman,R.W., Davis,R.W., Azarani,A., Schlossman,S.F., Duke-Cohan,J.S. and Barsh,G.S.
The mouse mahogany locus encodes a transmembrane form of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gunn,T.M., Miller,K.A., He,L., Hyman,R.W., Davis,R.W., Azarani,A., Direct Submission
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                                                                                                                                                                                                                                                                                       /note="transmembrane-region site"
6879. 6957
/gene="mg"
                                                                                                                                                                                                                                                                                                                                join(1870. .1931,6879. .6957)
                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="2"
                                                                                                                                                                                                                                                                                                                                                       /gene="mg"
                                                                                                                                                                                                                                                                                                                                                                          clone="BAC 389B9"
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          Glu 60 is replaced by Gln, Pro 361 by Ser, Met 362 by Leu and Ser
377 by Thr (nucleotide changes are not specified in [2]).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The open reading frame in the cDNA segs, derived from a different wild-type strain differs at four positions from that of the genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Moses,K., Elis,M.C. and Rubin,G.M.
The glass gene encodes a zinc-finger protein required by Drosophila photoreceptor cells
Nature 340..(6234)._531-535_(1989)...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (19-JUL-1989) Moses K., Howard Hughes Medical Institute,
Department of Biochemistry, University of California, Room 539 LSA,
Perkeley California 94720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7981 to 9044)
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1 (bases 1 to 9954)
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                                                                                                                                                                          /product="glass protein"
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/db_xref="GI:8016"
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RESULT 2 PARRN338 LOCUS LOCUS DEFINITION ACCESSION VERSION VERSION VERSION VERSION ORGANISM SOURCE ORGANISM REFERENCE AUTHORS TITLE	Query Matc Best Local Matches Qy 1 ga L Ja	RESULT 1 A98413 LOCUS DEFINITION ACCESSION VERSION KEYNORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE GRITHE GRITHE BASE COUNT ORIGIN	\$
PARRN23S 2893 bp DNA BCT Pseudomonas aeruginosa gene for 23S ribosomal Y00432 1 GI:45420 23S ribosomal RNA; ribosomal DNA. Pseudomonas aeruginosa. Pseudomonas aeruginosa Bacteria; Proteobacteria; gamma subdivision; Pseudomonas 1 (bases 1 to 2893) Ulbrich, N. Direct Submission	n 100.0%; Score 20; DB 5; Le Similarity 100.0%; Pred. No. 6.8; 20; Conservative 0; Mismatches 0; taggotgggtgtgtaagc 20	A98413 20 bp DNA PAT A98413 GI:6781514 unidentified. unidentifiedd. uniclassifiedd. 1 (bases 1 to 20) ROIfs, A. and Braeuer, A. AMINO ACID SEQUENCES AND METHOD FOR ISOLATING TYPE GENUS PSEDDOMONAS Patent: WO 9912949-A 18-MAR-1999; ROLFS ARNDT (DE); BRAEUER ANJA (DE) LOCATION/QUALIFIERS POTGANIST (DE) COTGANIST—"unidentified" /db_xref="taxon:33644" 4 a 2 c 9 9	18.4 92.0 2905 2 AF053963 18.4 92.0 2905 2 SEU77927 18.4 92.0 2906 2 SEU77921 18.4 92.0 2906 2 SEU77923 18.4 92.0 2906 2 SEU77923 18.4 92.0 2906 2 SEU77923 18.4 92.0 2906 2 SEU77924 18.4 92.0 2907 5 E16366 18.4 92.0 2907 5 E16367 18.4 92.0 2908 2 SEU77920 18.4 92.0 2908 2 SEU77926 18.4 92.0 3029 1 CSPLSURR 18.4 92.0 5203 2 TCOTRINH 18.4 92.0 5679 2 AF134704 18.4 92.0 5679 2 AF134704 18.4 92.0 6560 1 AB035923 18.4 92.0 6811 1 AB035923 18.4 92.0 6811 1 AB035924
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2 (bases 1 to 2893)
7 Toschka, H.Y., Hopfi, P., Ludwig, W., Schleifer, K.H., Ulbrich, N.
                                                                                                                                                                                                                                                                                               Christensen,H.
Direct Submission
Direct Submission
Submitted (12-NOV-1996) Veterinary Microbiology, Royal Veterinary
and Agricultural University, Bulowsvej 13, Frederiksberg 1870,
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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Complete nucleotide sequence of a 23S ribosomal RNA gene from Pseudomonas aeruginosa
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Christensen, H., Nordentoft, S. and Olsen, J.E.
Christensen, H., Nordentoft, S. and Olsen, J.E.
Phylogenetic relationships of Salmonella based on rRNA sequences
Int. J. Syst. Bacteriol. 48 Pt 2, 605-610 (1998)
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